Amendments to the claims:

1. (Currently Amended) A method for screening for transcription factor modulators, the method comprising:

forming a plurality of test samples by contacting samples of cells with different agents; and

for each test sample, identifying which of a plurality of different activated transcription factors are present by

taking a library of double stranded ~~transcription factor~~ nucleic acid probes, the transcription factor probes each comprising a predetermined recognition sequence capable of binding to an activated transcription factor, ~~the recognition sequence~~ and varying within the library for binding to different activated transcription factors,

contacting the ~~different~~ test sample with the library of double stranded DNA probes under conditions where ~~DNA~~ nucleic acid probe - transcription factor complexes are formed between the ~~DNA~~ nucleic acid probes and activated transcription factors present in the test ~~samples~~ sample,

isolating the ~~transcription factor~~ nucleic acid probes from the ~~transcription factor~~ nucleic acid probe-transcription factor complexes formed, and

~~identifying which transcription factor probes in the library formed complexes by taking an array of immobilized hybridization probes capable of hybridizing to at least one of the strands of the different double stranded transcription factor probes in the library and~~ contacting the isolated ~~transcription factor~~ nucleic acid probes with ~~the~~ an array of immobilized hybridization probes under conditions suitable for hybridization of the strands of the different double stranded ~~transcription factor~~ nucleic acid probes to the hybridization probes in the array, and

comparing the activated transcription factors present in the test sample with a control sample of cells not contacted with any of the different agents, the difference in the presence of transcription factors between the test and control sample being indicative of the transcription modulation by the agent contacted with the test sample; and

comparing the activated transcription factors present in the different test samples.

2. (Currently Amended) ~~A~~ The method according to claims 1 wherein at least 1% of the double stranded nucleic acid probes in the library have recognition sequences greater than 35 base pairs in length.

3. (Currently Amended) ~~A~~ The method according to claims 1 wherein at least 1% of the double stranded nucleic acid probes in the library have recognition sequences greater than 40 base pairs in length.

4. (Currently Amended) ~~A~~ The method according to claims 1 wherein at least 1% of the double stranded nucleic acid probes in the library have recognition sequences greater than 45 base pairs in length.

5. (Currently Amended) ~~A~~ The method according to claims 1 wherein at least 5% of the double stranded nucleic acid probes in the library have recognition sequences greater than 35 base pairs in length.

6. (Currently Amended) ~~A~~ The method according to claims 1 wherein at least 5% of the double stranded nucleic acid probes in the library have recognition sequences greater than 40 base pairs in length.

7. (Currently Amended) ~~A~~ The A method according to claims 1 wherein at least 5% of the double stranded nucleic acid probes in the library have recognition sequences greater than 45 base pairs in length.

8. (Currently Amended) ~~A~~ The A method according to claims 1 wherein ~~the library comprises probes having~~ each of the recognition sequences has between 20 and 40 base pairs in length.

9. (Currently Amended) ~~A~~ The A method according to claims 1 wherein ~~the library comprises probes having~~ each of the recognition sequences has between 25 and 35 base pairs in length.

10. (Currently Amended) ~~A~~ The A method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 5 different DNA recognition sequences.

11. (Currently Amended) ~~A~~ The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 10 different DNA recognition sequences.

12. (Currently Amended) ~~A~~ The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 20 different DNA recognition sequences.

13. (Currently Amended) ~~A~~ The A method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 50 different DNA recognition sequences.

14. (Currently Amended) ~~A~~ The method according to claims 1 wherein the library comprises DNA recognition sequences for at least 5 different types of cells.

15. (Currently Amended) ~~A~~ The A method according to claims 1 wherein ~~the library comprises~~ the DNA recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from at least 10 different types of cells.

16. (Currently Amended) ~~A~~ The method according to claims 1 wherein ~~the library comprises DNA~~ the recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from malignant, benign, and normal cell types.

17. (Currently Amended) ~~A~~ The A method according to claims 1 wherein ~~the binding regions of the transcription factor probes~~ each of the immobilized hybridization probes on the array ~~comprise~~ comprises at least two copies of a ~~compliment~~ complement to a portion of a recognition sequence comprised on the ~~transcription factor~~ nucleic acid probe.

18. (New) The method according to claim 1, wherein the recognition sequences comprised on the nucleic acid probes are predetermined to bind to two or more transcription factors selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E1, NF-E2, NFκB, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE.

19. (New) The method according to claim 1, wherein the recognition sequences comprised on the nucleic acid probes are predetermined to bind to two or more transcription factors selected from the group consisting of NF-E1, NFκB, Ets, Ap1, p53 and c-Myb.